

IN THE CLAIMS

1-5 (Cancelled)

Q8 6 (Currently Amended). The peptide of Claim ~~5~~75, wherein the N-terminus is amidated and the C-terminus is acylated.

7 (Cancelled)

Q9 8 (Currently Amended). The peptide of Claim ~~3~~68, wherein the protein kinase is a member of a protein kinase family selected from the group of families consisting of G protein-coupled receptor kinases, cyclin dependent kinases, Src family kinases, endothelial growth factor receptor kinases, fibroblast growth factor receptor kinases, Tyk/Jak kinases, insulin receptor kinases, ~~TGF α~~ TGF β receptor kinases, activin receptor-like kinases, neurotrophin receptor kinases, I-kappa B kinases, discoidin domain receptor kinases, and integrin-linked kinase.

9 (Original). The peptide of Claim 8 wherein the protein kinase is a G protein-coupled kinase selected from the group consisting of bARK1, bARK2, GRK1, GRK4, GRK5 and GRK6.

10 (Original). The peptide of Claim 8 wherein the protein kinase is a cyclin dependent kinase selected from the group consisting of CDK2, CDK4 and CDK6.

11 (Original). The peptide of Claim 8 wherein the protein kinase is a Src family kinase selected from the group

consisting of c-Src, c-Yes, Fyn, C-Fgr, Lyn, Hck, Lck, Csk and Matk.

12 (Original). The peptide of Claim 8 wherein the protein kinase is an endothelial growth factor receptor kinase selected from the group consisting of Tie, Tek, PDGFR-b, PDGFR-a, Flt1, Flt4 and Flk1.

13 (Original). The peptide of Claim 8 wherein the protein kinase is a fibroblast growth factor receptor kinase selected from the group consisting of Flg, Bek, FGFR-3 and FGFR-4.

14 (Original). The peptide of Claim 8 wherein the protein kinase is a Tyk/Jak kinase selected from the group consisting of Jak1, Jak2, Jak3 and Tyk2.

15 (Original). The peptide of Claim 8 wherein the protein kinase is a discoidin domain receptor kinase selected from the group consisting of DDR1 and DDR2.

210 16 (Currently amended). The peptide of Claim 8, wherein the protein kinase is a ~~TGF α~~ -TGF β receptor kinase selected from the group consisting of ~~TGF β RI~~TGF β RII, ACTRIIA and ACTRIIB.

17 (Original). The peptide of Claim 8 wherein the protein kinase is an activin receptor-like kinase selected from the group consisting of ALK1, ALK2, ALK3, ALK4, ALK5 and ALK6.

18 (Original). The peptide of Claim 8 wherein the protein kinase is a neurotrophin receptor kinase selected from the group consisting of Trk, TrkB, and TrkC.

19 (Original). The peptide of Claim 8 wherein the protein kinase is ILK.

20 (Original). The peptide of Claim 8 wherein the protein kinase is IRK.

21 (Original). The peptide of Claim 8 wherein protein kinase is an I-kappa B kinase selected from the group consisting of IKK-1 and IKK-2.

22 (Cancelled)

23 (Currently Amended). The peptide of Claim ~~3-68~~,
wherein the peptide has the sequence of SEQ ID NO:95, SEQ ID
NO:96, SEQ ID NO:97, SEQ ID NO:98, SEQ ID NO:99, SEQ ID
NO:100, SEQ ID NO:101, SEQ ID NO:102, SEQ ID NO:103, SEQ ID
NO:104, SEQ ID NO:105, SEQ ID NO:106, SEQ ID NO:107, SEQ ID
NO:108, SEQ ID NO:109, SEQ ID NO:110, SEQ ID NO:111, SEQ ID
all NO:112, SEQ ID NO:113, SEQ ID NO:114 SEQ ID NO:115, SEQ ID
NO:116, SEQ ID NO:117, SEQ ID NO:118, SEQ ID NO:119, SEQ ID
NO:120, SEQ ID NO:121, SEQ ID NO:122, SEQ ID NO:123, SEQ ID
NO:124, SEQ ID NO:125, SEQ ID NO:126, SEQ ID NO:127, SEQ ID
NO:128, SEQ ID NO:129, SEQ ID NO:130, SEQ ID NO:131, SEQ ID
NO:132, SEQ ID NO:133, SEQ ID NO:134, SEQ ID NO:135, SEQ ID
NO:136, SEQ ID NO:137, SEQ ID NO:138, SEQ ID NO:139, SEQ ID

NO:140, SEQ ID NO:141, SEQ ID NO:142, SEQ ID NO:143, SEQ ID
NO:144, SEQ ID NO:145, SEQ ID NO:146, SEQ ID NO:147, SEQ ID
NO:148, SEQ ID NO:149, SEQ ID NO:150, SEQ ID NO:151, SEQ ID
NO:152, SEQ ID NO:153, SEQ ID NO:154, SEQ ID NO:155, SEQ ID
NO:156, SEQ ID NO:157, SEQ ID NO:158, SEQ ID NO:159, SEQ ID
NO:160, SEQ ID NO:161, SEQ ID NO:162, SEQ ID NO:163, SEQ ID
NO:164, SEQ ID NO:165, SEQ ID NO:166, SEQ ID NO:167, SEQ ID
NO:168, SEQ ID NO:169, or SEQ ID NO:170.

24 (Currently Amended). A peptide having the

sequence of SEQ ID NO:95, SEQ ID NO:96, SEQ ID NO:97, SEQ ID
NO:98, SEQ ID NO:99, SEQ ID NO:100, SEQ ID NO:101, SEQ ID
NO:102, SEQ ID NO:103, SEQ ID NO:104, SEQ ID NO:105, SEQ ID
NO:106, SEQ ID NO:107, SEQ ID NO:108, SEQ ID NO:109, SEQ ID
NO:110, SEQ ID NO:111, SEQ ID NO:112, SEQ ID NO:113, SEQ ID
NO:114, SEQ ID NO:115, SEQ ID NO:116, SEQ ID NO:117, SEQ ID
NO:118, SEQ ID NO:119, SEQ ID NO:120, SEQ ID NO:121, SEQ ID
NO:122, SEQ ID NO:123, SEQ ID NO:124, SEQ ID NO:125, SEQ ID
NO:126, SEQ ID NO:127, SEQ ID NO:128, SEQ ID NO:129, SEQ ID
NO:130, SEQ ID NO:131, SEQ ID NO:132, SEQ ID NO:133, SEQ ID
NO:134, SEQ ID NO:135, SEQ ID NO:136, SEQ ID NO:137, SEQ ID
NO:138, SEQ ID NO:139, SEQ ID NO:140, SEQ ID NO:141, SEQ ID
NO:142, SEQ ID NO:143, SEQ ID NO:144, SEQ ID NO:145, SEQ ID
NO:146, SEQ ID NO:147, SEQ ID NO:148, SEQ ID NO:149, SEQ ID
NO:150, SEQ ID NO:151, SEQ ID NO:152, SEQ ID NO:153, SEQ ID

Q11 NO:154, SEQ ID NO:155, SEQ ID NO:156, SEQ ID NO:157, SEQ ID NO:158, SEQ ID NO:159, SEQ ID NO:160, SEQ ID NO:161, SEQ ID NO:162, SEQ ID NO:163, SEQ ID NO:164, SEQ ID NO:165, SEQ ID NO:166, SEQ ID NO:167, SEQ ID NO:168, SEQ ID NO:169, or SEQ ID NO:170, with the proviso that any one amino acid residue in the peptide can vary, ~~being any naturally occurring~~be substituted by another amino acid residue or ~~conservatively substituted functional~~amino acid residue analog thereof.

25 (Original). A peptide consisting of a sequence of amino acids AA₁ through AA₂₃ or a subsequence thereof comprising at least five amino acids, wherein:

AA₁ is selected from the group consisting of leucine, methionine, isoleucine and valine;

AA₂ is selected from the group consisting of aspartic acid, threonine, glutamic acid, serine and an aliphatic, substituted aliphatic, benzyl, substituted benzyl, aromatic or substituted aromatic ester of a glutamic acid or aspartic acid;

AA₃ is selected from the group consisting of leucine, isoleucine, methionine and valine;

AA₄ is selected from the group consisting of methionine, isoleucine, leucine and valine;

AA₅ is selected from the group consisting of asparagine and glutamine;

AA₆ is selected from the group consisting of glycine and alanine;

AA₇ is selected from the group consisting of glycine and alanine;

AA₈ is selected from the group consisting of aspartic acid, glutamic acid and an aliphatic, substituted aliphatic, benzyl, substituted benzyl, aromatic or substituted aromatic ester of a glutamic acid or aspartic acid;

AA₉ is selected from the group consisting of leucine, isoleucine, methionine and valine;

AA₁₀ is selected from the group consisting of histidine, arginine and lysine;

AA₁₁ is selected from the group consisting of tyrosine, phenylalanine and tryptophan;

AA₁₂ is histidine;

AA₁₃ is selected from the group consisting of leucine, isoleucine, methionine and valine;

AA₁₄ is selected from the group consisting of serine, tyrosine, threonine, phenylalanine and tryptophan;

AA₁₅ is selected from the group consisting of glutamine, asparagine and histidine;

AA₁₆ is selected from the group consisting of histidine, valine, leucine, methionine and isoleucine;

AA₁₇ is selected from the group consisting of glycine, aspartic acid, glutamic acid, alanine and an aliphatic, substituted aliphatic, benzyl, substituted benzyl, aromatic or substituted aromatic ester of a glutamic acid or aspartic acid;

AA₁₈ is selected from the group consisting of valine, glutamic acid, asparagine, glutamine, isoleucine, leucine, methionine, aspartic acid and an aliphatic, substituted aliphatic, benzyl, substituted benzyl, aromatic or substituted aromatic ester of a glutamic acid or aspartic acid;

AA₁₉ is selected from the group consisting of pheynylalanine, aspartic acid, proline, alanine, tryptophan, tyrosine, glutamic acid, glycine and an aliphatic, substituted aliphatic, benzyl, substituted benzyl, aromatic or substituted aromatic ester of a glutamic acid or aspartic acid;

AA₂₀ is selected from the group consisting of asparagine, glycine, glutamine and alanine;

AA₂₁ is selected from the group consisting of proline, phenylalanine, tryptophan and tyrosine;

AA₂₂ is selected from the group consisting of glycine and alanine; and

AA₂₃ is selected from the group consisting of phenylalanine, tryptophan and tyrosine.

26 (Original). The peptide of Claim 25 wherein the sequence AA₁ through AA₂₃ or a subsequence thereof corresponds to a sequence of the α D region of a G protein-coupled receptor kinase selected from the group consisting of SEQ ID NO:18, SEQ ID NO:19, SEQ ID NO:20, SEQ ID NO:21 and SEQ ID NO:22 or a subsequence thereof, with the proviso that any two amino acids in the sequence AA₁ through AA₂₃ or the subsequence thereof can vary as set forth in Claim 25.

27 (Original). The peptide of Claim 25 wherein the sequence AA₁ through AA₂₃ or a subsequence thereof corresponds to the sequence or a subsequence of the α D region of a G protein-coupled receptor kinase selected from the group consisting of SEQ ID NO:18, SEQ ID NO:19, SEQ ID NO:20, SEQ ID NO:21 and SEQ ID NO:22, with the proviso that any one amino acid in the sequence AA₁ through AA₂₃ or the subsequence thereof can vary as set forth in Claim 25.

28 (Original). A peptide consisting of a sequence of amino acids AA₁ through AA₂₀ or a subsequence thereof comprising at least seven amino acids, wherein:

AA₁ is selected from the group consisting of phenylalanine, tryptophan and tyrosine;

AA₂ is selected from the group consisting of glutamic acid, aspartic acid and an aliphatic, substituted aliphatic,

benzyl, substituted benzyl, aromatic or substituted aromatic ester of glutamic acid or aspartic acid;

AA₃ is selected from the group consisting of phenylalanine, histidine, tryptophan and tyrosine;

AA₄ is selected from the group consisting of leucine, valine, isoleucine and methionine;

AA₅ is selected from the group consisting of histidine, aspartic acid, glutamic acid, and an aliphatic, substituted aliphatic, benzyl, substituted benzyl, aromatic or substituted aromatic ester of glutamic acid or aspartic acid;

AA₆ is selected from the group consisting of glutamine and asparagine;

AA₇ is selected from the group consisting of aspartic acid, glutamic acid and an aliphatic, substituted aliphatic, benzyl, substituted benzyl, aromatic or substituted aromatic ester of glutamic acid or aspartic acid;

AA₈ is selected from the group consisting of leucine, isoleucine, methionine and valine;

AA₉ is selected from the group consisting of lysine, arginine, threonine and serine;

AA₁₀ is selected from the group consisting of lysine, threonine, arginine and serine;

AA₁₁ is selected from the group consisting of phenylalanine, tyrosine and tryptophan;

AA₁₂ is selected from the group consisting of methionine, leucine, isoleucine and valine;

AA₁₃ is selected from the group consisting of aspartic acid, glutamic acid and an aliphatic, substituted aliphatic, benzyl, substituted benzyl, aromatic or substituted aromatic ester of glutamic acid or aspartic acid;

AA₁₄ is selected from the group consisting of alanine, lysine, arginine and glycine;

AA₁₅ is selected from the group consisting of valine, serine, alanine, isoleucine, leucine, methionine and threonine;

AA₁₆ is selected from the group consisting of alanine, proline and glycine;

AA₁₇ is selected from the group consisting of leucine, proline, glutamic acid, isoleucine, methionine, valine, aspartic acid and an aliphatic, substituted aliphatic, benzyl, substituted benzyl, aromatic or substituted aromatic ester of glutamic acid or aspartic acid;

AA₁₈ is selected from the group consisting of threonine, proline and serine;

AA₁₉ is selected from the group consisting of glycine and alanine; and

AA₂₀ is selected from the group consisting of isoleucine, leucine, valine and methionine.

29 (Original). The peptide of Claim 28 wherein the sequence AA₁ through AA₂₀ or a subsequence thereof corresponds to a sequence of the α D region of a cyclin dependent kinase selected from the group consisting of SEQ ID NO:35, SEQ ID NO:36 and SEQ ID NO:37 or a subsequence thereof, with the proviso that any two amino acids in the sequence AA₁ through AA₂₀ or the subsequence thereof can vary as set forth in Claim 28.

30 (Original). The peptide of Claim 28 wherein the sequence AA₁ through AA₂₀ or a subsequence thereof corresponds to a sequence of the α D region of a cyclin dependent kinase selected from the group consisting of SEQ ID NO:35, SEQ ID NO:36 and SEQ ID NO:37 or a subsequence thereof, with the proviso that any one amino acid in the sequence AA₁ through AA₂₀ or the subsequence thereof can vary as set forth in Claim 28.

31 (Original). A peptide consisting of a sequence of amino acids AA₁ through AA₂₁ or a subsequence thereof comprising at least seven amino acids, wherein:

AA₁ is selected from the group consisting of threonine, methionine, serine, isoleucine, leucine and valine;

AA₂ is selected from the group consisting of glutamic acid, aspartic acid and an aliphatic, substituted aliphatic,

benzyl, substituted benzyl, aromatic or substituted aromatic ester of glutamic acid or aspartic acid;

AA₃ is selected from the group consisting of phenylalanine, tyrosine, histidine and tryptophan;

AA₄ is selected from the group consisting of methionine, valine, isoleucine and leucine;

AA₅ is selected from the group consisting of serine, asparagine, cysteine, alanine, glutamic acid, threonine, glutamine, aspartic acid, glycine and an aliphatic, substituted aliphatic, benzyl, substituted benzyl, aromatic or substituted aromatic ester of glutamic acid or aspartic acid;

AA₆ is selected from the group consisting of lysine, histidine, asparagine, arginine and glutamine;

AA₇ is selected from the group consisting of glycine and alanine;

AA₈ is selected from the group consisting of serine, asparagine, threonine and glutamine;

AA₉ is selected from the group consisting of leucine, isoleucine, methionine and valine;

AA₁₀ is selected from the group consisting of leucine, valine, isoleucine and methionine;

AA₁₁ is selected from the group consisting of aspartic acid, asparagine, glutamic acid, glutamine and an aliphatic, substituted aliphatic, benzyl, substituted benzyl,

aromatic or substituted aromatic ester of glutamic acid or aspartic acid;

AA₁₂ is selected from the group consisting of phenylalanine, tyrosine and tryptophan;

AA₁₃ is selected from the group consisting of leucine, isoleucine, methionine and valine;

AA₁₄ is selected from the group consisting of lysine and arginine;

AA₁₅ is selected from the group consisting of glycine, glutamic acid, aspartic acid, asparagine, serine, threonine, glutamine, alanine and an aliphatic, substituted aliphatic, benzyl, substituted benzyl, aromatic or substituted aromatic ester of glutamic acid or aspartic acid;

AA₁₆ is selected from the group consisting of glutamic acid, glycine, proline, aspartic acid, arginine, lysine, alanine and an aliphatic, substituted aliphatic, benzyl, substituted benzyl, aromatic or substituted aromatic ester of glutamic acid or aspartic acid;

AA₁₇ is selected from the group consisting of threonine, serine, aspartic acid, glutamic acid, glycine, alanine and an aliphatic, substituted aliphatic, benzyl, substituted benzyl, aromatic or substituted aromatic ester of glutamic acid or aspartic acid;

AA₁₈ is selected from the group consisting of glycine, arginine, lysine and alanine;

AA₁₉ is selected from the group consisting of lysine, arginine, glutamine, glycine, serine, isoleucine, alanine, asparagine, threonine, leucine, methionine and valine;

AA₂₀ is selected from the group consisting of tyrosine, alanine, aspartic acid, lysine, valine, leucine, phenylalanine, tryptophan, glutamic acid, arginine, isoleucine, methionine, glycine and an aliphatic, substituted aliphatic, benzyl, substituted benzyl, aromatic or substituted aromatic ester of glutamic acid or aspartic acid; and

AA₂₁ is selected from the group consisting of leucine, valine, glutamine, isoleucine, methionine and asparagine.

32 (Original). The peptide of Claim 31 wherein the sequence AA₁ through AA₂₁ or a subsequence thereof corresponds to the sequence of the α D region of a Src family kinase selected from the group consisting of SEQ ID NO:38, SEQ ID NO:39, SEQ ID NO:40, SEQ ID NO:41, SEQ ID NO:42, SEQ ID NO:43, SEQ ID NO:44, SEQ ID NO:45 and SEQ ID NO:46 or a subsequence thereof, with the proviso that any two amino acids in the sequence AA₁ through AA₂₁ or the subsequence thereof can vary as set forth in Claim 31.

33 (Original). The peptide of Claim 31 wherein the sequence AA₁ through AA₂₁ or a subsequence thereof corresponds to the sequence of the α D region of a Src family kinase selected from the group consisting of SEQ ID NO:38, SEQ ID NO:39, SEQ ID NO:40, SEQ ID NO:41, SEQ ID NO:42, SEQ ID NO:43, SEQ ID NO:44, SEQ ID NO:45 and SEQ ID NO:46 or a subsequence thereof, with the proviso that any one amino acid in the sequence AA₁ through AA₂₁ or the subsequence thereof can vary as set forth in Claim 31.

34 (Original). A peptide consisting of a sequence of amino acids AA₁ through AA₃₉ or a subsequence thereof comprising at least seven amino acids, wherein:

AA₁ is selected from the group consisting of isoleucine, threonine, valine, leucine, methionine and serine;

AA₂ is selected from the group consisting of glutamic acid, aspartic acid and an aliphatic, substituted aliphatic, benzyl, substituted benzyl, aromatic or substituted aromatic ester of glutamic acid or aspartic acid;

AA₃ is selected from the group consisting of tyrosine, phenylalanine and tryptophan;

AA₄ is selected from the group consisting of alanine, cysteine, serine, threonine and glycine;

AA₅ is selected from the group consisting of glycine, arginine, phenylalanine, lysine, tryptophan and tyrosine;

AA₆ is selected from the group consisting of tyrosine, histidine, phenylalanine and tryptophan;

AA₇ is selected from the group consisting of glycine and alanine;

AA₈ is selected from the group consisting of asparagine, aspartic acid, glutamine, glutamic acid and an aliphatic, substituted aliphatic, benzyl, substituted benzyl, aromatic or substituted aromatic ester of glutamic acid or aspartic acid;

AA₉ is selected from the group consisting of leucine, isoleucine, methionine and valine;

AA₁₀ is selected from the group consisting of leucine, valine, serine, isoleucine, methionine and threonine;

AA₁₁ is selected from the group consisting of aspartic acid, asparagine, threonine, glutamic acid, glutamine, serine and an aliphatic, substituted aliphatic, benzyl, substituted benzyl, aromatic or substituted aromatic ester of glutamic acid or aspartic acid;

AA₁₂ is selected from the group consisting of phenylalanine, tyrosine and tryptophan;

AA₁₃ is selected from the group consisting of leucine, isoleucine, methionine and valine;

AA₁₄ is selected from the group consisting of arginine, histidine and lysine;

AA₁₅ is selected from the group consisting of lysine, arginine, serine, alanine, glycine and threonine;

AA₁₆ is selected from the group consisting of serine, asparagine, lysine, threonine, glutamine and arginine;

AA₁₇ is selected from the group consisting of arginine and lysine;

AA₁₈ is selected from the group consisting of valine, histidine, aspartic acid, asparagine, isoleucine, leucine, methionine, glutamic acid, glutamine and an aliphatic, substituted aliphatic, benzyl, substituted benzyl, aromatic or substituted aromatic ester of glutamic acid or aspartic acid;

AA₁₉ is selected from the group consisting of leucine, threonine, serine, alanine, glutamic acid, isoleucine, methionine, valine, aspartic acid, glycine and an aliphatic, substituted aliphatic, benzyl, substituted benzyl, aromatic or substituted aromatic ester of glutamic acid or aspartic acid;

AA₂₀ is selected from the group consisting of glutamic acid, phenylalnine, aspartic acid, tryptophan, tyrosine and an aliphatic, substituted aliphatic, benzyl, substituted benzyl, aromatic or substituted aromatic ester of glutamic acid or aspartic acid;

AA₂₁ is selected from the group consisting of threonine, leucine, phenylalanine, serine, valine, isoleucine, methionine, tryptophan and tyrosine;

AA₂₂ is selected from the group consisting of aspartic acid, glutamine, serine, leucine, proline, glutamic acid, asparagine, threonine, isoleucine, methionine, valine and an aliphatic, substituted aliphatic, benzyl, substituted benzyl, aromatic or substituted aromatic ester of glutamic acid or aspartic acid;

AA₂₃ is selected from the group consisting of proline, histidine, asparagine, cysteine, tyrosine, glutamine, phenylalanine, tryptophan, and serine;

AA₂₄ is selected from the group consisting of alanine, histidine, lysine, arginine and glycine;

AA₂₅ is selected from the group consisting of phenylalanine, serine, proline, aspartic acid, glutamic acid, tryptophan, tyrosine, threonine and an aliphatic, substituted aliphatic, benzyl, substituted benzyl, aromatic or substituted aromatic ester of glutamic acid or aspartic acid;

AA₂₆ is selected from the group consisting of alanine, aspartic acid, glutamic acid, lysine, arginine, glycine and an aliphatic, substituted aliphatic, benzyl, substituted benzyl, aromatic or substituted aromatic ester of glutamic acid or aspartic acid;

AA₂₇ is selected from the group consisting of arginine, isoleucine, lysine, alanine, serine, glycine, leucine, methionine, valine and threonine;

AA₂₈ is selected from the group consisting of glutamic acid, alanine, arginine, proline, leucine, aspartic acid, lysine, isoleucine, methionine, valine, glycine and an aliphatic, substituted aliphatic, benzyl, substituted benzyl, aromatic or substituted aromatic ester of glutamic acid or aspartic acid;

AA₂₉ is selected from the group consisting of histidine, asparagine, arginine, lysine, glutamic acid, glutamine, aspartic acid and an aliphatic, substituted aliphatic, benzyl, substituted benzyl, aromatic or substituted aromatic ester of glutamic acid or aspartic acid;

AA₃₀ is selected from the group consisting of glycine, serine, proline, lysine, methionine, glutamine, phenylalanine, threonine, arginine, isoleucine, leucine, valine, asparagine, tryptophan, tyrosine and alanine;

AA₃₁ is selected from the group consisting of threonine, proline, glutamic acid, arginine, serine, aspartic acid, lysine and an aliphatic, substituted aliphatic, benzyl, substituted benzyl, aromatic or substituted aromatic ester of glutamic acid or aspartic acid;

AA₃₂ is selected from the group consisting of serine, alanine, aspartic acid, lysine, arginine, glycine, threonine, glutamic acid and an aliphatic, substituted aliphatic, benzyl, substituted benzyl, aromatic or substituted aromatic ester of glutamic acid or aspartic acid;

AA₃₃ is selected from the group consisting of threonine, glutamic acid, isoleucine, lysine, phenylalanine, serine, aspartic acid, leucine, methionine, valine, arginine, tryptophan, tyrosine and an aliphatic, substituted aliphatic, benzyl, substituted benzyl, aromatic or substituted aromatic ester of glutamic acid or aspartic acid;

AA₃₄ is selected from the group consisting of leucine, phenylalanine, glutamic acid, arginine, aspartic acid, isoleucine, methionine, valine, tryptophan, tyrosine, lysine and an aliphatic, substituted aliphatic, benzyl, substituted benzyl, aromatic or substituted aromatic ester of glutamic acid or aspartic acid;

AA₃₅ is selected from the group consisting of tyrosine, glycine, lysine, alanine, phenylalanine, tryptophan and arginine;

AA₃₆ is selected from the group consisting of serine, leucine, methionine, valine, threonine, and isoleucine;

AA₃₇ is selected from the group consisting of asparagine, glutamic acid, valine, glycine, glutamine,

aspartic acid, isoleucine, leucine, methionine, alanine and an aliphatic, substituted aliphatic, benzyl, substituted benzyl, aromatic or substituted aromatic ester of glutamic acid or aspartic acid;

AA₃₈ is selected from the group consisting of alanine, proline, glutamic acid, aspartic acid, glycine and an aliphatic, substituted aliphatic, benzyl, substituted benzyl, aromatic or substituted aromatic ester of glutamic acid or aspartic acid;

AA₃₉ is selected from the group consisting of leucine, alanine, glycine, isoleucine, methionine and valine.

35 (Original). The peptide of Claim 34, wherein the sequence AA₁ through AA₃₉ or a subsequence thereof corresponds to the sequence of the α D region of an endothelial growth factor receptor kinase selected from the group consisting of SEQ ID NO:49, SEQ ID NO:50, SEQ ID NO:55, SEQ ID NO:56, SEQ ID NO:57, SEQ ID NO:58 and SEQ ID NO:59 or a subsequence thereof, with the proviso that any two amino acids in the sequence AA₁ through AA₃₉ or the subsequence thereof can vary as set forth in Claim 34.

36 (Original). The peptide of Claim 34 wherein the sequence AA₁ through AA₃₉ or a subsequence thereof corresponds to the sequence of the α D region of an endothelial growth factor receptor kinase selected from the group consisting of

SEQ ID NO:49, SEQ ID NO:50, SEQ ID NO:55, SEQ ID NO:56, SEQ ID NO:57, SEQ ID NO:58 and SEQ ID NO:59 or a subsequence thereof, with the proviso that any one amino acid in the sequence AA₁ through AA₃₉ or the subsequence thereof can vary as set forth in Claim 34.

37 (Original). A peptide consisting of a sequence of amino acids AA₁ through AA₃₄ or a subsequence thereof comprising at least seven amino acids, wherein:

AA₁ is selected from the group consisting of valine, isoleucine, leucine and methionine;

AA₂ is selected from the group consisting of glutamic acid, aspartic acid and an aliphatic, substituted aliphatic, benzyl, substituted benzyl, aromatic or substituted aromatic ester of glutamic acid or aspartic acid;

AA₃ is selected from the group consisting of tyrosine, cysteine, phenylalanine, tryptophan and serine;

AA₄ is selected from the group consisting of alanine and glycine;

AA₅ is selected from the group consisting of serine, alanine, threonine and glycine;

AA₆ is selected from the group consisting of lysine and arginine;

AA₇ is selected from the group consisting of glycine and alanine;

AA₈ is selected from the group consisting of asparagine and glutamine;

AA₉ is selected from the group consisting of leucine, isoleucine, methionine and valine;

AA₁₀ is selected from the group consisting of arginine and lysine;

AA₁₁ is selected from the group consisting of glutamic acid, aspartic acid and an aliphatic, substituted aliphatic, benzyl, substituted benzyl, aromatic or substituted aromatic ester of glutamic acid or aspartic acid;

AA₁₂ is selected from the group consisting of tyrosine, phenylalanine and tryptophan;

AA₁₃ is selected from the group consisting of leucine, isoleucine, methionine and valine;

AA₁₄ is selected from the group consisting of glutamine, arginine, asparagine and lysine;

AA₁₅ is selected from the group consisting of alanine and glycine;

AA₁₆ is selected from the group consisting of arginine and lysine;

AA₁₇ is selected from the group consisting of arginine and lysine;

AA₁₈ is proline;

AA₁₉ is proline;

AA₂₀ is selected from the group consisting of glycine and alanine;

AA₂₁ is selected from the group consisting of leucine, methionine, proline, isoleucine and valine;

AA₂₂ is selected from the group consisting of glutamic acid, aspartic acid and an aliphatic, substituted aliphatic, benzyl, substituted benzyl, aromatic or substituted aromatic ester of glutamic acid or aspartic acid;

AA₂₃ is selected from the group consisting of tyrosine, leucine, phenylalanine, tryptophan, isoleucine, methionine and valine;

AA₂₄ is selected from the group consisting of cysteine, serine and threonine;

AA₂₅ is selected from the group consisting of tyrosine, phenylalanine, proline and tryptophan;

AA₂₆ is selected from the group consisting of asparagine, aspartic acid, glutamine, glutamic acid and an aliphatic, substituted aliphatic, benzyl, substituted benzyl, aromatic or substituted aromatic ester of glutamic acid or aspartic acid;

AA₂₇ is selected from the group consisting of proline, isoleucine, threonine, glycine, leucine, methionine, valine, serine and alanine;

AA₂₈ is selected from the group consisting of serine, asparagine, cysteine, proline, threonine and glutamine;

AA₂₉ is selected from the group consisting of histidine, arginine and lysine;

AA₃₀ is selected from the group consisting of asparagine, valine, proline, serine, glutamine, isoleucine, leucine, methionine and threonine;

AA₃₁ is selected from the group consisting of proline, serine and threonine;

AA₃₂ is selected from the group consisting of glutamic acid, glycine, aspartic acid, alanine and an aliphatic, substituted aliphatic, benzyl, substituted benzyl, aromatic or substituted aromatic ester of glutamic acid or aspartic acid;

AA₃₃ is selected from the group consisting of glutamine, proline and asparagine; and

AA₃₄ is selected from the group consisting of leucine, methionine, isoleucine and valine.

38 (Original). The peptide of Claim 37 wherein the sequence AA₁ through AA₃₄ or a subsequence thereof corresponds to the sequence of the α D region of a fibroblast growth factor receptor kinase selected from the group consisting of SEQ ID NO:51, SEQ ID NO:52, SEQ ID NO:53 and SEQ ID NO:54 or a subsequence thereof, with the proviso that any two amino acids

in the sequence AA₁ through AA₃₄ or the subsequence thereof can vary as set forth in Claim 37.

39 (Original). The peptide of Claim 37 wherein the sequence AA₁ through AA₃₄ or a subsequence thereof corresponds to the sequence of the α D region of a fibroblast growth factor receptor kinase selected from the group consisting of SEQ ID NO:51, SEQ ID NO:52, SEQ ID NO:53 and SEQ ID NO:54 or a subsequence thereof, with the proviso that any one amino acid in the sequence AA₁ through AA₃₄ or the subsequence thereof can vary as set forth in Claim 37.

40 (Original). A peptide consisting of a sequence of amino acids AA₁ through AA₂₀ or a subsequence thereof comprising at least five amino acids, wherein:

AA₁ is selected from the group consisting of methionine, isoleucine, leucine and valine;

AA₂ is selected from the group consisting of glutamic acid, aspartic acid and an aliphatic, substituted aliphatic, benzyl, substituted benzyl, aromatic or substituted aromatic ester of glutamic acid or aspartic acid;

AA₃ is selected from the group consisting of phenylalanine, tyrosine, and tryptophan;

AA₄ is selected from the group consisting of leucine, isoleucine, methionine and valine;

AA₅ is proline;

AA₆ is selected from the group consisting of serine, tyrosine, threonine, phenylalanine, tryptophan, leucine and isoleucine;

AA₇ is selected from the group consisting of glycine and alanine;

AA₈ is selected from the group consisting of serine, cysteine and threonine;

AA₉ is selected from the group consisting of leucine, isoleucine, methionine and valine;

AA₁₀ is selected from the group consisting of lysine and arginine;

AA₁₁ is selected from the group consisting of glutamic acid, aspartic acid and an aliphatic, substituted aliphatic, benzyl, substituted benzyl, aromatic or substituted aromatic ester of glutamic acid or aspartic acid;

AA₁₂ is selected from the group consisting of tyrosine, phenylalanine and tryptophan;

AA₁₃ is selected from the group consisting of leucine, isoleucine, methionine and valine;

AA₁₄ is selected from the group consisting of proline, glutamine, and asparagine;

AA₁₅ is selected from the group consisting of lysine and arginine;

AA₁₆ is selected from the group consisting of asparagine, histidine and glutamine;

AA₁₇ is selected from the group consisting of lysine, arginine, serine and threonine;

AA₁₈ is selected from the group consisting of asparagine, glutamic acid, alanine, glutamine, aspartic acid, glycine, isoleucine, leucine and an aliphatic, substituted aliphatic, benzyl, substituted benzyl, aromatic or substituted aromatic ester of glutamic acid or aspartic acid;

AA₁₉ is selected from the group consisting of lysine and arginine; and

AA₂₀ is selected from the group consisting of isoleucine, leucine, methionine and valine.

41 (Original). The peptide of Claim 40 wherein the sequence AA₁ through AA₂₀ or a subsequence thereof corresponds to the sequence of the α D region of a Tyk/Jak kinase selected from the group consisting of SEQ ID NO:73, SEQ ID NO:74, SEQ ID NO:75 and SEQ ID NO:76 or a subsequence thereof, with the proviso that any two amino acids in the sequence AA₁ through AA₂₀ or the subsequence thereof can vary as set forth in Claim 40.

42 (Original). The peptide of Claim 40 wherein the sequence AA₁ through AA₂₀ or a subsequence thereof corresponds to the sequence of the α Dregion of a Tyk/Jak kinase selected

from the group consisting of SEQ ID NO:73, SEQ ID NO:74, SEQ ID NO:75 and SEQ ID NO:76 or a subsequence thereof, with the proviso that any one amino acid in the sequence AA₁ through AA₂₀ or the subsequence thereof can vary as set forth in Claim 40.

43 (Original). A peptide consisting of a sequence of amino acids AA₁ through AA₃₁ or a subsequence thereof comprising at least five amino acids, wherein:

AA₁ is selected from the group consisting of methionine, isoleucine, leucine and valine;

AA₂ is selected from the group consisting of glutamic acid, aspartic acid and an aliphatic, substituted aliphatic, benzyl, substituted benzyl, aromatic or substituted aromatic ester of glutamic acid or aspartic acid;

AA₃ is selected from the group consisting of leucine, isoleucine, methionine and valine;

AA₄ is selected from the group consisting of methionine, isoleucine, leucine and valine;

AA₅ is selected from the group consisting of alanine and glycine;

AA₆ is histidine;

AA₇ is selected from the group consisting of glycine and alanine;

AA₈ is selected from the group consisting of aspartic acid, glutamic acid and an aliphatic, substituted aliphatic, benzyl, substituted benzyl, aromatic or substituted aromatic ester of glutamic acid or aspartic acid;

AA₉ is selected from the group consisting of leucine, isoleucine, methionine and valine;

AA₁₀ is selected from the group consisting of lysine and arginine;

AA₁₁ is selected from the group consisting of serine and threonine;

AA₁₂ is selected from the group consisting of tyrosine, phenylalanine and tryptophan;

AA₁₃ is selected from the group consisting of leucine, isoleucine, methionine and valine;

AA₁₄ is selected from the group consisting of arginine and lysine;

AA₁₅ is selected from the group consisting of serine and threonine;

AA₁₆ is selected from the group consisting of leucine, isoleucine, methionine and valine;

AA₁₇ is selected from the group consisting of arginine and lysine;

AA₁₈ is proline;

AA₁₉ is selected from the group consisting of glutamic acid, aspartic acid and an aliphatic, substituted aliphatic, benzyl, substituted benzyl, aromatic or substituted aromatic ester of glutamic acid or aspartic acid;

AA₂₀ is selected from the group consisting of alanine and glycine;

AA₂₁ is selected from the group consisting of glutamic acid, aspartic acid and an aliphatic, substituted aliphatic, benzyl, substituted benzyl, aromatic or substituted aromatic ester of glutamic acid or aspartic acid;

AA₂₂ is selected from the group consisting of asparagine and glutamine;

AA₂₃ is selected from the group consisting of asparagine and glutamine;

AA₂₄ is proline;

AA₂₅ is selected from the group consisting of glycine and alanine;

AA₂₆ is selected from the group consisting of arginine and lysine;

AA₂₇ is proline;

AA₂₈ is proline;

AA₂₉ is proline;

AA₃₀ is selected from the group consisting of threonine and serine; and

AA₃₁ is selected from the group consisting of leucine, isoleucine, methionine and valine, with the proviso that the peptide is not represented by the sequence MAHGDLKSYLRSLRPEAENNP (SEQ ID NO:171).

44 (Original). The peptide of Claim 43 wherein the sequence AA₁ through AA₃₁ or a subsequence thereof corresponds to the sequence of the α D region of SEQ ID NO:82 or a subsequence thereof, with the proviso that any two amino acids in the sequence AA₁ through AA₃₁ or the subsequence thereof can vary as set forth in Claim 43.

45 (Original). The peptide of Claim 43 wherein the sequence AA₁ through AA₃₁ or a subsequence thereof corresponds to the sequence of the α D region of SEQ ID NO:82 or a subsequence thereof, with the proviso that any one amino acid in the sequence AA₁ through AA₃₁ or the subsequence thereof can vary as set forth in Claim 43.

46 (Original). A peptide consisting of a sequence of amino acids AA₁ through AA₁₈ or a subsequence thereof comprising at least seven amino acids, wherein:

AA₁ is selected from the group consisting of threonine and serine;

AA₂ is selected from the group consisting of alanine and glycine;

AA₃ is selected from the group consisting of phenylalanine, tryptophan and tyrosine;

AA₄ is histidine;

AA₅ is selected from the group consisting of alanine, glutamic acid, aspartic acid, glycine and an aliphatic, substituted aliphatic, benzyl, substituted benzyl, aromatic or substituted aromatic ester of glutamic acid or aspartic acid;

AA₆ is selected from the group consisting of lysine and arginine;

AA₇ is selected from the group consisting of glycine and alanine;

AA₈ is selected from the group consisting of asparagine, serine, glutamine and threonine;

AA₉ is selected from the group consisting of leucine, isoleucine, methionine and valine;

AA₁₀ is selected from the group consisting of glutamine, serine and threonine;

AA₁₁ is selected from the group consisting of glutamic acid, aspartic acid and an aliphatic, substituted aliphatic, benzyl, substituted benzyl, aromatic or substituted aromatic ester of glutamic acid or aspartic acid;

AA₁₂ is selected from the group consisting of tyrosine, phenylalanine and tryptophan;

AA₁₃ is selected from the group consisting of leucine, isoleucine, methionine and valine;

AA₁₄ is selected from the group consisting of threonine, lysine, serine and arginine;

AA₁₅ is selected from the group consisting of arginine, alanine, glycine and lysine;

AA₁₆ is selected from the group consisting of histidine, asparagine and glutamine;

AA₁₇ is selected from the group consisting of valine, isoleucine, leucine and methionine; and

AA₁₈ is selected from the group consisting of isoleucine, valine, leucine and methionine.

47 (Original). The peptide of Claim 46 wherein the sequence AA₁ through AA₁₈ or a subsequence thereof corresponds to the sequence of the α D region of a TGF β receptor kinase selected from the group consisting of SEQ ID NO:83, SEQ ID NO:84 and SEQ ID NO:85 or a subsequence thereof, with the proviso that any two amino acids in the sequence AA₁ through AA₁₈ or the subsequence thereof can vary as set forth in Claim 46.

48 (Original). The peptide of Claim 46 wherein the sequence AA₁ through AA₁₈ or a subsequence thereof corresponds to the sequence of the α D region of a TGF β receptor kinase selected from the group consisting of SEQ ID NO:83, SEQ ID

NO:84 and SEQ ID NO:85 or a subsequence thereof, with the proviso that any one amino acid in the sequence AA₁ through AA₁₈ or the subsequence thereof can vary as set forth in Claim 46.

49 (Original). A peptide consisting of a sequence of amino acids AA₁ through AA₁₈ or a subsequence thereof comprising at least seven amino acids, wherein:

AA₁ is selected from the group consisting of threonine and serine;

AA₂ is selected from the group consisting of histidine, aspartic acid, glutamic acid and an aliphatic, substituted aliphatic, benzyl, substituted benzyl, aromatic or substituted aromatic ester of glutamic acid or aspartic acid;

AA₃ is selected from the group consisting of tyrosine, phenylalanine and tryptophan;

AA₄ is histidine;

AA₅ is selected from the group consisting of glutamic acid, aspartic acid and an aliphatic, substituted aliphatic, benzyl, substituted benzyl, aromatic or substituted aromatic ester of glutamic acid or aspartic acid;

AA₆ is selected from the group consisting of histidine, methionine, asparagine, isoleucine, leucine, valine and glutamine;

AA₇ is selected from the group consisting of glycine and alanine;

AA₈ is selected from the group consisting of serine and threonine;

AA₉ is selected from the group consisting of leucine, isoleucine, methionine and valine;

AA₁₀ is selected from the group consisting of tyrosine, phenylalanine and tryptophan;

AA₁₁ is selected from the group consisting of aspartic acid, glutamic acid and an aliphatic, substituted aliphatic, benzyl, substituted benzyl, aromatic or substituted aromatic ester of glutamic acid or aspartic acid;

AA₁₂ is selected from the group consisting of phenylalanine, tyrosine and tryptophan;

AA₁₃ is selected from the group consisting of leucine, isoleucine, methionine and valine;

AA₁₄ is selected from the group consisting of glutamine, lysine, asparagine and arginine;

AA₁₅ is selected from the group consisting of arginine, leucine, cysteine, serine, lysine, isoleucine, methionine, valine and threonine;

AA₁₆ is selected from the group consisting of glutamine, threonine, alanine, tyrosine, asparagine, serine, phenylalanine, tryptophan and glycine;

AA₁₇ is selected from the group consisting of threonine and serine; and

AA₁₈ is selected from the group consisting of leucine, valine, isoleucine and methionine.

50 (Original). The peptide of Claim 49 wherein the sequence AA₁ through AA₁₈ or a subsequence thereof corresponds to the sequence of the α D region of an activin receptor-like kinase selected from the group consisting of SEQ ID NO:86, SEQ ID NO:87, SEQ ID NO:88, SEQ ID NO:89 and SEQ ID NO:90 or a subsequence thereof, with the proviso that any two amino acids in the sequence AA₁ through AA₁₈ or the subsequence thereof can vary as set forth in Claim 49.

51 (Original). The peptide of Claim 49 wherein the sequence AA₁ through AA₁₈ or a subsequence thereof corresponds to the sequence of the α D region of an activin receptor-like kinase selected from the group consisting of SEQ ID NO:86, SEQ ID NO:87, SEQ ID NO:88, SEQ ID NO:89 and SEQ ID NO:90 or a subsequence thereof, with the proviso that any one amino acid in the sequence AA₁ through AA₁₈ or the subsequence thereof can vary as set forth in Claim 49.

52 (Original). A peptide consisting of a sequence of amino acids AA₁ through AA₃₄ or a subsequence thereof comprising at least five amino acids, wherein:

AA₁ is selected from the group consisting of phenylalanine, tryptophan and tyrosine;

AA₂ is selected from the group consisting of glutamic acid, aspartic acid and an aliphatic, substituted aliphatic, benzyl, substituted benzyl, aromatic or substituted aromatic ester of glutamic acid or aspartic acid;

AA₃ is selected from the group consisting of tyrosine, phenylalanine and tryptophan;

AA₄ is selected from the group consisting of methionine, isoleucine, leucine and valine;

AA₅ is selected from the group consisting of arginine and lysine;

AA₆ is histidine;

AA₇ is selected from the group consisting of glycine and alanine;

AA₈ is selected from the group consisting of aspartic acid, glutamic acid and an aliphatic, substituted aliphatic, benzyl, substituted benzyl, aromatic or substituted aromatic ester of glutamic acid or aspartic acid;

AA₉ is selected from the group consisting of leucine, isoleucine, methionine and valine;

AA₁₀ is selected from the group consisting of asparagine and glutamine;

AA₁₁ is selected from the group consisting of arginine and lysine;

AA₁₂ is selected from the group consisting of phenylalanine, tryptophan and tyrosine;

AA₁₃ is selected from the group consisting of leucine, isoleucine, methionine and valine;

AA₁₄ is selected from the group consisting of arginine and lysine;

AA₁₅ is selected from the group consisting of serine, alanine, threonine and glycine;

AA₁₆ is histidine;

AA₁₇ is selected from the group consisting of glycine and alanine;

AA₁₈ is proline;

AA₁₉ is selected from the group consisting of aspartic acid, glutamic acid and an aliphatic, substituted aliphatic, benzyl, substituted benzyl, aromatic or substituted aromatic ester of glutamic acid or aspartic acid;

AA₂₀ is selected from the group consisting of alanine and glycine;

AA₂₁ is selected from the group consisting of lysine, valine, methionine, arginine, isoleucine and leucine;

AA₂₂ is selected from the group consisting of leucine, isoleucine, methionine and valine;

AA₂₃ is selected from the group consisting of leucine, methionine, isoleucine and valine;

AA₂₄ is selected from the group consisting of alanine, valine, isoleucine, leucine, methionine and glycine;

AA₂₅ is selected from the group consisting of glycine, glutamic acid, aspartic acid, alanine and an aliphatic, substituted aliphatic, benzyl, substituted benzyl, aromatic or substituted aromatic ester of glutamic acid or aspartic acid;

AA₂₆ is selected from the group consisting of glycine and alanine;

AA₂₇ is selected from the group consisting of glutamic acid, asparagine, glutamine, aspartic acid and an aliphatic, substituted aliphatic, benzyl, substituted benzyl, aromatic or substituted aromatic ester of glutamic acid or aspartic acid;

AA₂₈ is selected from the group consisting of aspartic acid, proline, glutamic acid and an aliphatic, substituted aliphatic, benzyl, substituted benzyl, aromatic or substituted aromatic ester of glutamic acid or aspartic acid;

AA₂₉ is selected from the group consisting of valine, proline, arginine, isoleucine, leucine, methionine and lysine;

AA₃₀ is selected from the group consisting of alanine, threonine, glutamine, serine, asparagine and glycine;

AA₃₁ is selected from the group consisting of proline, glutamic acid, alanine, aspartic acid, glycine and an aliphatic, substituted aliphatic, benzyl, substituted benzyl, aromatic or substituted aromatic ester of glutamic acid or aspartic acid;

AA₃₂ is selected from the group consisting of proline, glycine and alanine;

AA₃₃ is selected from the group consisting of leucine, glutamic acid, isoleucine, methionine, valine, aspartic acid and an aliphatic, substituted aliphatic, benzyl, substituted benzyl, aromatic or substituted aromatic ester of glutamic acid or aspartic acid; and

AA₃₄ is selected from the group consisting of leucine, isoleucine, methionine and valine.

53 (Original). The peptide of Claim 52 wherein the sequence AA₁ through AA₃₄ or a subsequence thereof corresponds to the sequence of the α D region of a neurotrophic receptor kinase selected from the group consisting of SEQ ID NO:68, SEQ ID NO:69 and SEQ ID NO:70 or a subsequence thereof, with the proviso that any two amino acids in the sequence AA₁ through AA₃₄ or the subsequence thereof can vary as set forth in Claim 52.

54 (Original). The peptide of Claim 52 wherein the sequence AA₁ through AA₁₈ or a subsequence thereof corresponds

to the sequence of the α D region of a neurotrophic receptor kinase selected from the group consisting of SEQ ID NO:68, SEQ ID NO:69 and SEQ ID NO:70 or a subsequence thereof, with the proviso that any one amino acid in the sequence AA₁ through AA₃₁ or the subsequence thereof can vary as set forth in Claim 52.

55 (Original). A peptide consisting of a sequence of amino acids AA₁ through AA₂₁ or a subsequence thereof comprising at least five amino acids, wherein:

AA₁ is selected from the group consisting of threonine and serine;

AA₂ is histidine

AA₃ is selected from the group consisting of tryptophan, phenylalanine and tyrosine;

AA₄ is selected from the group consisting of methionine, isoleucine, leucine and methionine;

AA₅ is proline;

AA₆ is selected from the group consisting of tyrosine, phenylalanine and tryptophan;

AA₇ is selected from the group consisting of glycine and alanine;

AA₈ is selected from the group consisting of serine and threonine;

AA₉ is selected from the group consisting of leucine, isoleucine, methionine and valine;

AA₁₀ is selected from the group consisting of tyrosine, phenylalanine and tryptophan;

AA₁₁ is selected from the group consisting of asparagine and glutamine;

AA₁₂ is selected from the group consisting of valine, isoleucine, leucine and methionine;

AA₁₃ is selected from the group consisting of leucine, isoleucine, methionine and valine;

AA₁₄ is histidine;

AA₁₅ is selected from the group consisting of glutamic acid, aspartic acid and an aliphatic, substituted aliphatic, benzyl, substituted benzyl, aromatic or substituted aromatic ester of glutamic acid or aspartic acid;

AA₁₆ is selected from the group consisting of glycine and alanine;

AA₁₇ is selected from the group consisting of threonine and serine;

AA₁₈ is selected from the group consisting of asparagine and glutamine;

AA₁₉ is selected from the group consisting of phenylalanine, tryptophan and tyrosine;

AA₂₀ is selected from the group consisting of valine, isoleucine, leucine and methionine; and

AA₂₁ is selected from the group consisting of valine, isoleucine, leucine and methionine.

56 (Original). The peptide of Claim 55 wherein the sequence AA₁ through AA₂₁ or a subsequence thereof corresponds to the sequence of the α D region of SEQ ID NO:93 or a subsequence thereof, with the proviso that any two amino acids in the sequence AA₁ through AA₂₁ or the subsequence thereof can vary as set forth in Claim 55.

57 (Original). The peptide of Claim 55 wherein the sequence AA₁ through AA₂₁ or a subsequence thereof corresponds to the sequence of the α D region of SEQ ID NO:93 or a subsequence thereof, with the proviso that any one amino acid in the sequence AA₁ through AA₂₁ or the subsequence thereof can vary as set forth in Claim 55.

58 (Original). A peptide consisting of a sequence of amino acids AA₁ through AA₂₂ or a subsequence thereof comprising at least five amino acids, wherein:

AA₁ is selected from the group consisting of methionine, isoleucine, leucine and valine;

AA₂ is selected from the group consisting of glutamic acid, aspartic acid and an aliphatic, substituted aliphatic,

benzyl, substituted benzyl, aromatic or substituted aromatic ester of glutamic acid or aspartic acid;

AA₃ is selected from the group consisting of tyrosine, phenylalanine and tryptophan;

AA₄ is selected from the group consisting of cysteine and serine;

AA₅ is selected from the group consisting of serine, glutamine, threonine and asparagine;

AA₆ is selected from the group consisting of glycine and alanine;

AA₇ is selected from the group consisting of glycine and alanine;

AA₈ is selected from the group consisting of aspartic acid, glutamic acid and an aliphatic, substituted aliphatic, benzyl, substituted benzyl, aromatic or substituted aromatic ester of glutamic acid or aspartic acid;

AA₉ is selected from the group consisting of leucine, isoleucine, methionine and valine;

AA₁₀ is selected from the group consisting of arginine and lysine;

AA₁₁ is selected from the group consisting of lysine and asparagine;

AA₁₂ is selected from the group consisting of leucine, tyrosine, isoleucine, methionine, valine, phenylalanine and tryptophan;

AA₁₃ is selected from the group consisting of leucine, isoleucine, methionine and valine;

AA₁₄ is selected from the group consisting of asparagine and glutamine;

AA₁₅ is selected from the group consisting of lysine, glutamine, arginine and asparagine;

AA₁₆ is selected from the group consisting of proline, phenylalanine, tryptophan and tyrosine;

AA₁₇ is selected from the group consisting of glutamic acid, aspartic acid and an aliphatic, substituted aliphatic, benzyl, substituted benzyl, aromatic or substituted aromatic ester of glutamic acid or aspartic acid;

AA₁₈ is selected from the group consisting of asparagine and glutamine;

AA₁₉ is selected from the group consisting of cysteine and serine;

AA₂₀ is selected from the group consisting of cysteine and serine;

AA₂₁ is selected from the group consisting of glycine and alanine; and

AA₂₂ is selected from the group consisting of leucine, isoleucine, methionine and valine.

59 (Original). The peptide of Claim 58 wherein the sequence AA₁ through AA₂₂ or a subsequence thereof corresponds to the sequence of the α D region of an I-kappa B kinase selected from the group consisting of SEQ ID NO:79 and SEQ ID NO:80 or a subsequence thereof, with the proviso that any two amino acids in the sequence AA₁ through AA₂₂ or the subsequence thereof can vary as set forth in Claim 58.

60 (Original). The peptide of Claim 58 wherein the sequence AA₁ through AA₂₂ or a subsequence thereof corresponds to the sequence of the α D region of an I-kappa B kinase selected from the group consisting of SEQ ID NO:79 and SEQ ID NO:80 or a subsequence thereof, with the proviso that any one amino acid in the sequence AA₁ through AA₂₂ or the subsequence thereof can vary as set forth in Claim 58.

61 (Currently Amended). A method of identifying a peptide which modulates the activity of a protein kinase, comprising ~~the steps of~~:

612 a) providing a peptide, referred to as a "test peptide", ~~consisting~~ comprising a peptide derivative of the α D region ~~or a subsequence of the α D region~~ of said protein kinase and having from ~~seven~~ five to about thirty amino acids

acid residues or ~~conservatively substituted functional~~amino acid residue analogs thereof;

b) incubating the test peptide with cells having one or more cellular activities controlled by a protein kinase, under conditions suitable for assessing activity of the protein kinase; and

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c) assessing activity of the protein kinase, wherein greater or lesser activity compared with the cells grown without incubation of the test peptide indicates that the test peptide modulates activity of the protein kinase.

62 (Original). The method of Claim 61, wherein the activity of the protein kinase is assessed by measuring the rate of survival or proliferation of said cells in tissue culture.

63 (Currently Amended). A method of modulating the activity of a protein kinase in a subject, comprising administering a therapeutically effective amount of a peptide ~~consisting comprising~~ a peptide derivative of the α D region or ~~a subsequence of the α D region~~ of a protein kinase, wherein:

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a) said peptide has between five and about thirty amino ~~acids~~ acid residues or ~~conservatively substituted functional~~ amino acid residue analogs; and

b) said peptide modulates activity of the protein kinase.

64 (Currently Amended). A method of detecting a ligand that binds to the α D region of a protein kinase, comprising:

a) providing a peptide ~~set forth by~~ comprising a peptide derivative of the α D region or a subsequence of the α D region of said protein kinase, said peptide derivative having at least ~~seven~~ five ~~amino acids~~ acid residues or ~~conservatively substituted functional~~ amino acid residue analogs thereof;

Q13 b) incubating said peptide with a sample, to be tested for the presence of said ligand, for a time sufficient for said ligand to bind to said peptide; and

c) detecting any said ligand-said peptide binding pair that has been formed in ~~step b~~, wherein the presence of said ligand-said peptide binding pair establishes the existence of said ligand in said sample.

65 (Original). The method of Claim 64 further comprising:

d) separating said ligand from said peptide;
and

e) determining the structure of said ligand, thereby identifying said ligand.

66-67 (Cancelled)

68 (New). A peptide capable of modulating the activity of a protein kinase having a structure that includes the twelve subdomains and nine alpha helices that are characteristic of the protein kinase superfamily, consisting of:

514 a) an α D region peptide consisting of a sequence of about 20 amino acid residues of the protein kinase Subdomain V and the beginning of Subdomain VI, beginning at the end of the b5 beta sheet and extending through the D helix and the following loop to the beginning of helix E, which amino acids correspond to a continuous stretch of the prototypical PKA-C α in positions 120-139 of the PKA-C α , and which α D region peptide modulates the activity of the protein kinase;

b) a subsequence peptide consisting of a subsequence of a) consisting of at least five contiguous amino acids thereof, which subsequence peptide modulates the activity of the protein kinase;

c) a modified sequence peptide having a modified sequence of a) or b) in which up to two residues are each substituted by another amino acid residue or amino acid residue analog other than one which is identical to the one being substituted except that a functional group in the side chain is functionalized with a protecting group, which

modified sequence peptide modulates the activity of the protein kinase;

d) a protected peptide a), b) or c) in which the N-terminus and/or the C-terminus is protected by a protecting group and/or one or more side chains of the amino acid residues of the peptide of a), b) or c) have been functionalized with a protecting group, which protected peptide modulates the activity of the protein kinase; or

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cont. e) a cyclized peptide of a), b), c) or d) which has been cyclized, which cyclized peptide modulates the activity of the protein kinase.

69 (New). A peptide in accordance with Claim 68, consisting of an α D region peptide of a); a peptide of a) in which the N-terminus and/or the C-terminus is protected by a protecting group, which protected peptide modulates the activity of the protein kinase; or a peptide of a) which has been cyclized, which cyclized peptide modulates the activity of the protein kinase.

70 (New). A peptide in accordance with Claim 69, consisting of an α D region peptide of a).

71 (New). A peptide in accordance with Claim 68, consisting of a subsequence peptide of b); a peptide of b) in which the N-terminus and/or the C-terminus is protected by a protecting group, which protected peptide modulates the

activity of the protein kinase; or a peptide of b) which has been cyclized, which cyclized peptide modulates the activity of the protein kinase.

72 (New). A peptide in accordance with Claim 71, consisting of a subsequence peptide of b).

9/14 (at.)
73 (New). A peptide in accordance with Claim 68, consisting of a modified sequence peptide of c); a peptide of c) in which the N-terminus and/or the C-terminus is protected by a protecting group, which protected peptide modulates the activity of the protein kinase; or a peptide of c) which has been cyclized, which cyclized peptide modulates the activity of the protein kinase.

74 (New). A peptide in accordance with Claim 73, consisting of a modified peptide of c).

75 (New). A peptide in accordance with Claim 68, consisting of a protected peptide of d).

76 (New). A peptide in accordance with Claim 71, consisting of a cyclized peptide of e).

77 (New). A method in accordance with Claim 61, further including:

d) producing any test peptide which has been assessed in c) as modulating activity of the protein kinase.

78 (New). A method according to claim 61, wherein the "test peptide" is selected from the group consisting of:

i) an α D region peptide consisting of a sequence of about 20 amino acid residues of the protein kinase Subdomain V and the beginning of Subdomain VI, beginning at the end of the b5 beta sheet and extending through the D helix and the following loop to the beginning of helix E, which amino acids correspond to a continuous stretch of the prototypical PKA-C α in positions 120-139 of the PKA-C α ;

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cat. ii) a subsequence peptide consisting of a subsequence of i) consisting of at least five contiguous amino acids thereof;

iii) a modified sequence peptide having a modified sequence of i) or ii) in which at least one residue is each substituted by another amino acid residue or amino acid residue analog;

iv) a protected peptide i), ii) or iii) in which the N-terminus and/or the C-terminus is protected by a protecting group; or

v) a cyclized peptide of i), ii), iii) or iv) which has been cyclized, which cyclized peptide modulates the activity of the protein kinase.

79 (New). A method according to claim 78, wherein the modified sequence of iii) has up to two residues that are each substituted by another amino acid residue or amino acid residue analog.

80 (New). A method according to claim 63, wherein the peptide is selected from the group consisting of:

Am
(at). i) an α D region peptide consisting of a sequence of about 20 amino acid residues of the protein kinase Subdomain V and the beginning of Subdomain VI, beginning at the end of the b5 beta sheet and extending through the D helix and the following loop to the beginning of helix E, which amino acids correspond to a continuous stretch of the prototypical PKA-C α in positions 120-139 of the PKA-C α , and which α D region peptide modulates the activity of the protein kinase;

ii) a subsequence peptide consisting of a subsequence of i) consisting of at least five contiguous amino acids thereof, which subsequence peptide modulates the activity of the protein kinase

iii) a modified sequence peptide having a modified sequence of i) or ii) in which at least one residue is each substituted by another amino acid residue or amino acid residue analog, which modified sequence peptide modulates the activity of the protein kinase;

iv) a protected peptide i), ii) or iii) in which the N-terminus and/or the C-terminus is protected by a protecting group, which protected peptide modulates the activity of the protein kinase; or

v) a cyclized peptide of i), ii), iii) or iv) which has been cyclized, which cyclized peptide modulates the activity of the protein kinase.

81 (New). A method according to claim 80, wherein the modified sequence of iii) has up to two residues that are each substituted by another amino acid residue or amino acid residue analog.

82 (New). A method according to claim 64 wherein the peptide is selected from the group consisting of:

Q14
(cont.)
i) an α D region peptide consisting of a sequence of about 20 amino acid residues of the protein kinase Subdomain V and the beginning of Subdomain VI, beginning at the end of the b5 beta sheet and extending through the D helix and the following loop to the beginning of helix E, which amino acids correspond to a continuous stretch of the prototypical PKA-C α in positions 120-139 of the PKA-C α ;

ii) a subsequence peptide consisting of a subsequence of a) consisting of at least five contiguous amino acids thereof;

iii) a modified sequence peptide having a modified sequence of i) or ii) in which at least one residue is each substituted by another amino acid residue or amino acid residue analog;

iv) a protected peptide i), ii) or iii) in which the N-terminus and/or the C-terminus is protected by a protecting group; or

v) a cyclized peptide of i), ii), iii) or iv) which has been cyclized, which cyclized peptide modulates the activity of the protein kinase.

83 (New). A method according to claim 82, wherein the modified sequence of iii) has up to two residues that are each substituted by another amino acid residue or amino acid residue analog.

Q14
cont.
84 (New). A method in accordance with Claim 65, further comprising:

f) producing any said ligand identified in e).

85 (New). A peptide in accordance with claim 68, wherein at least one of the protecting groups of the protected peptide of d) is one that facilitates transport of the peptide into a cell.

86 (New). A peptide in accordance with claim 85, wherein said protecting group that facilitates transport of the peptide into a cell is one that reduces the hydrophilicity and increases the lipophilicity of the peptide.
